

Identification of selection signatures for response of American mink to Aleutian mink disease virus infection

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Introduction

- Aleutian disease (AD) is one of the most important health issues in the mink industry worldwide, leading to economic losses.
- Thus far, no effective vaccine or treatment is available for AD (1). However, selection for tolerant animals can be a feasible approach to control AD on mink farms.
- The objective of this study was to detect the genomic regions potentially under selection for response to Aleutian mink disease virus (AMDV) infection in American mink.

Methods

A total of 191 mink which were inoculated with a local strain of AMDV and survived until pelting were genotyped using genotyping-by-sequencing technique. The presence of viral DNA in the spleen samples were tested by polymerase chain reaction. After filtering, 47,800 SNPs at 171 individuals were used for further analyses. Signatures of selection for response to AMDV infection were detected using fixation index (F_{ST}) and nucleotide diversity ($\theta\pi$) statistics measured between negative and positive groups. The overlap of top 1% SNPs obtained from both F_{ST} and $\theta\pi$ scores were considered as potential selection signs. The gene ontology was performed using PANTHER 14.1.

Results

Integrated measurement of F_{ST} and $\theta\pi$ identified a total of 21 candidate regions containing 11 genes which were likely subjected to selection for viral clearance (Figure 1 and Table 1). Several identified genes were those that modulate immune system (*TCF4*), reproductive process (*CATSPERB*, *MAS1* and *IGF2R*), response to stimulus (*WNT11* and *MAS1*), and functions of heart (*TENM4* and *WNT11*) and liver (*IGF2R*). In addition, gene ontology showed that 63.6% of detected genes (seven) were involved in binding activities (Figure 2).

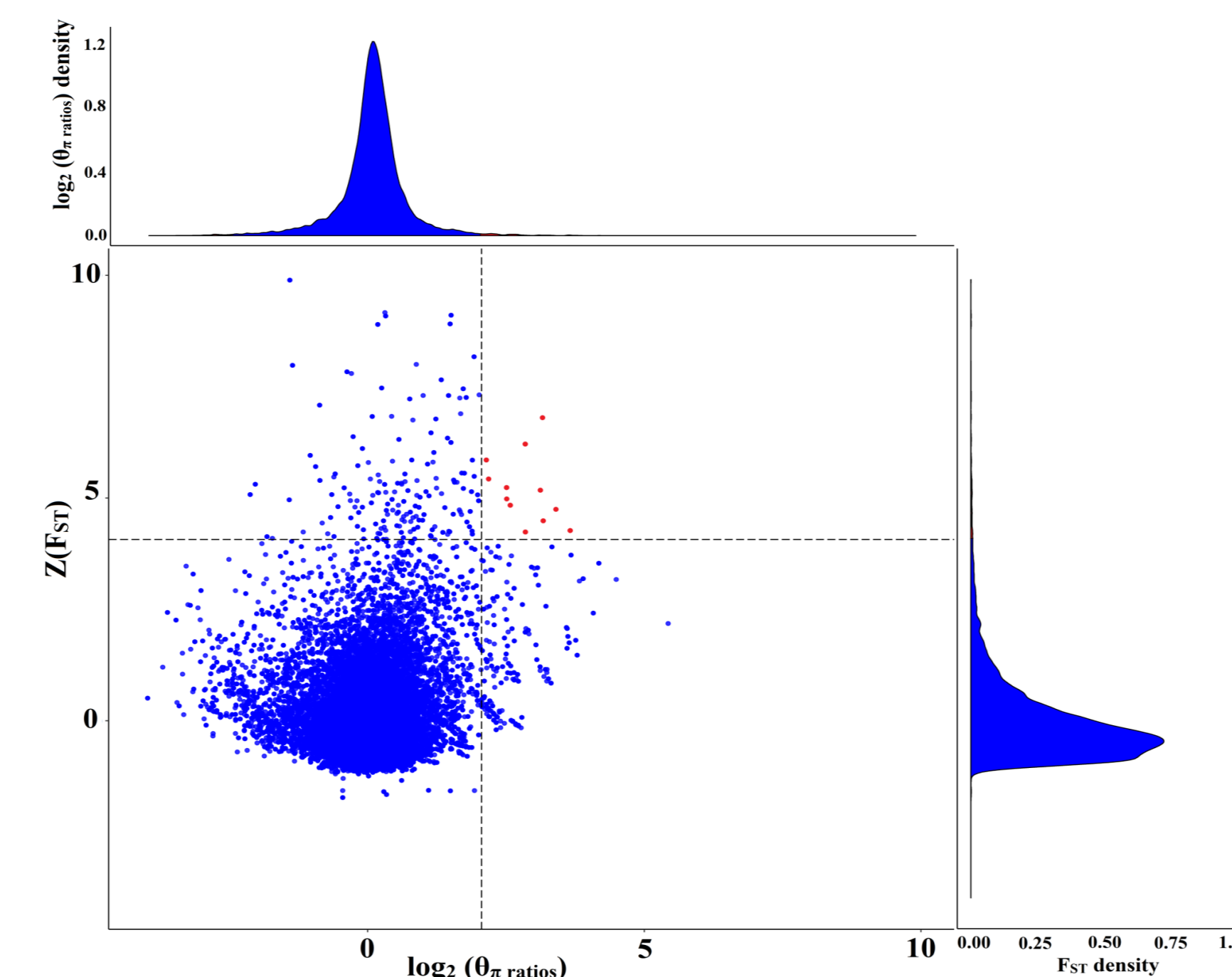


Figure 1. Distribution of $\theta\pi$ ratios ($\theta\pi_{\text{Negative}} / \theta\pi_{\text{Positive}}$) and $Z(F_{ST})$ values

Table 1. The candidate regions along with their positions using both $Z(F_{ST})$ and $\log_2(\theta_\pi \text{ ratio})$

Scaffolds	Start point	$Z(F_{ST})$	$\log_2(\theta_\pi \text{ ratio})$
1	4475001	5.17	3.12
1	4500001	5.17	3.12
1	4525001	5.17	3.12
1	23825001	5.85	2.14
1	23850001	5.85	2.14
1	24525001	4.24	2.85
1	24550001	4.24	2.85
5	16525001	4.84	2.57
5	22550001	6.21	2.84
6	13475001	4.27	3.66
6	13500001	4.27	3.66
6	19295001	4.74	3.40
6	19320001	4.70	3.40
7	5000001	4.49	3.17
7	5025001	4.49	3.17
7	7325001	5.23	2.51
7	19350001	5.43	2.18
7	19375001	5.43	2.18
7	19400001	5.43	2.18
8	13950001	4.98	2.51
8	21400001	6.80	3.16

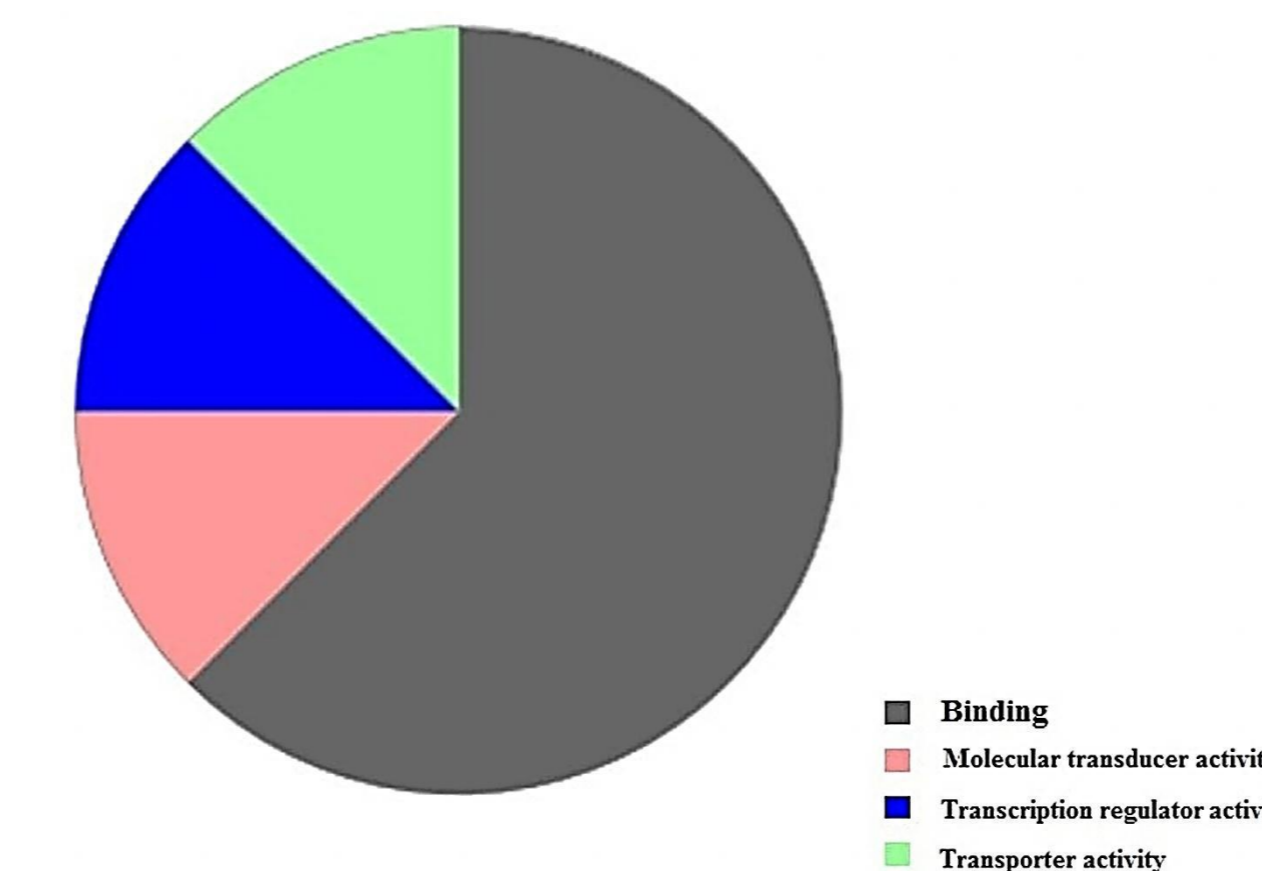


Figure 2. The pie chart of molecular functions attributed to candidate genes

Discussion

Selection for tolerant mink is certainly a feasible approach to control the AMDV infection on mink farms. Genomic selection can be applied as a useful breeding strategy to improve the economically important traits in the mink industry (2). Detection of numerous loci in this study implies that genomic selection would be an effective approach to increase the tolerance against AMDV infection in mink. However, further investigations would be required to validate the role of these putatively selected regions in AD control. The collection of suggested genes in this study presents a foundation for development of molecular approaches to unveil the response of mink to AMDV infection.

References

1. Liu, D. *et al.* Construction and immunogenicity analysis of whole-gene mutation DNA vaccine of Aleutian mink virus isolated virulent strain. *Viral immunol* **31**, 69-77 (2018).
2. Karimi, K. *et al.* Opportunities for genomic selection in American mink: A simulation study. *PLOS ONE* **14**, e0213873 (2019).

Acknowledgements

We would like to acknowledge P.P. Rupasinghe and L.F. Butler for technical assistance. Financial support was received from NSERC, Mitacs, Canada Mink Breeders Association, Nova Scotia Mink Breeders Association, and Agriculture and Agri-Food Canada.